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```

      [N-term] []          [ 2 ]      [ 3 ]      [ 4 ]
      + +      9          22 26      31 36      41 44
BLC   1  SVIGSDDRTRVTNNTTAYPYRAIVHISSSIGSCTGWMIGPKTVATA 45
      .          .          .          .          .

      []      []      [ 7 ]          [ 8 ]      { }
      *  50      56      62 65          77      83 86 90
BLC  46  GHCIYDTSSGSFAGTATVSPGRNGTSYPYGSVKSTRYFIPSGWRS 90
      .          .          .          .          .

      [ 9 ]      { }      []          [ 11 ]
      *  99 102 106 110 114          126 131
BLC  91  GNTNYDYGAIELSEPIGNTVGYFGYSYTTSSLVGTTVTISGYPGD 135
      .          .          .          .          .

      [ 12 ]      [13]          [ 14 ]
      142      151 156 +          *  171 177
BLC 136  KTAGTQWQHSGPIAISETYKLQYAMDTYGGQSGSPVFEQSSSRTN 180
      .          .          .          .          .

      [ 15 ]      [ 16 ]      { }
      182      192      201 208      219
BLC 181  CSGPCSLAVHTNGVYGGSSYNRGTRITKEVFDNLTNWKNSAQ 222
      .          .          .          .          .

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* Active site residue (47, 96, 167)

+ Calcium coordination residue (3, 5, 161)

[] Short strand (9-10, 50-51, 56-57, 114-115)

[] Long strand (22-26, 31-36, 41-44, 62-65, 77-83, 99-102,
126-131, 142-151, 156-159, 171-177, 182-192, 201-205)

{ } Helix (86-90, 106-110, 208-219)

Fig. 1

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BLC      .SVIGSDDRTRVTNTTAYPYRAIVHISSS*****IGSCTGWMIGPKTVA 43
CDJ31    .SVIGSDERTRVTNTTAYPYRAIVHISSS*****IGSCTGSLIGPKTVA
AC116    .SVIGSDERTRVTDTTAFPPYRAIVHISSS*****IGSCTGWLIGPKTVA

MIP      .VVIGDDGRTKVANTRVAPYNSIAYITFG*****GSSCTGTLIAPNKIL
JA96     .VVIGDDGRTKVTNTRVAPYNSIAYITFG*****GSSCTGTLIAPNKIL
BO32     .VVIGDDGRTKVANTRVAPYNSIAYTTFG*****GSSCTGTLIAPNKIL
          abcdef .

MPR      .SIIGTDERTRISSTTSFPYRATVQLSIKYPNTSSTYGCTGFLVNPNTVV
AA513    .VVIGDDGRRQVQNTSFMPFRALTYIEFG**NLTSTWSCSGGVIGTDLVV

BLC      TAGHCIYDTSSGSFAGTATVSPGRNGTSYPYGSVKSTRYFIPSGWR*SGN 92
CDJ31    TAGHCIYDTASGSFAGTATVSPGRNGSTYPYGSVTSTRYFIPSGYR*SGN
AC116    TAGHCVYDTASRSFAGTATVSPGRNGSAYPYGSVTSTRYFIPSGWQ*SGN
          a.

MIP      TNGHCVYNTASRSYSAKGSVYPGMNDSTAVNGSANMTEFYVPSPGYINTGA
JA96     TNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSANMTEFYVPSPGYINTGA
BO32     TNGHCVYNTASRSYSAKGSVYPGMNDSTAVNGSANMTEFYVPSPGYINTGA
          a.

MPR      TAGHCVY*SQDHGWASTITAAPGRNGSSYPYGTYSGMTFYSVKGWTESKD
AA513    TNAHCV*****EGSVLAGTVVPGMNNSQWAYGHYRVQTQIIYPDQYRNNGA

BLC      TNYDYGAIELS*****EPIGNTVGYFGYSYT*TSSLVGTTVTISGYPGDK 136
CDJ31    SNYDYGAIELS*****QPIGNTVGYFGYSYT*TSSLVGSSVTIIGYPGDK
AC116    SNYDYAAIELS*****QPIGNTVGYFGYSYT*ASSLAGAGVTISGYPGDK

MIP      SQYDFAVIKTD*****TNIGNTVGYRSIRQ**VTNLTGTTIKISGYPGDK
JA96     SQYDFAVIKTD*****TNIGNTVGYRSIRQ**VTNLTGTTIKISGYPGDK
BO32     SQYDFAVIKTD*****TNIGNTVGYRSIRQ**VTNLTGTTIKISGYPGDK
          abcde a .

MPR      TNYDYGAIKLN*****GSPGNTVGWYGYRTTNSSSPVGLSSSVTGFPCKD
AA513    SEFDYAILRVAPDSDGRHIGNRAGILSFTETGTVN*ENTFLRTYGYPGDK

BLC      T****AGTQWQHSGPIAISET*YKLQYAMDTYGGQSGSPVFEQSSSRTNC 181
CDJ31    T****SGTQWQMSGNIAVSET*YKLQYAITDYGGQSGSPVYEASSSRTNC
AC116    T****TGTQWQMSGTIAVSET*YKLQYAITDYGGQSGSPVYEKSSSRTNC
          abcd .

MIP      MRSTGKVSQWEMSGSVTREDT*NLAYYTIDTFSGNSGSAMLDQ*****
JA96     MRSTGKVSQWEMSGPVTREDT*NLAYYTIDTFSGNSGSAMLDQ*****
BO32     MRSTGKISQWEMSGPVTREDT*NLAYYMIDTFSGNSGSAMLDQ*****
          abcd a .

MPR      T****FGTMWSDTKPIRSAET*YKLTYYTDDTYGCQSGSPVYRNYSD****
AA513    ISETKLISLWGMVGRSDAFLHRDLLFYNMMDTYFGQSGSPVLN*****

BLC      NGPCSLAVHTNG**VYGGSSYNRGTRITKEVFDNLTNWKNNSAQ 222
CDJ31    SGPCSLAVHTNG**VYGGSSYNRGTRITKEVFDNLTNWKNNSAQ
AC116    SGPCSLAVHTNG**VYGGSSYNRGTRITKEVFDNFTSWKNNSAQ

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Fig. 2

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      .       .       .
MIP      *NQQIVGVHNAG***YSNGTINGGPKATAAFVEFINYAKAQ**
JA96     *NQQIVGVHNAG***YSNGTINGGPKATAAFVEFINYAKAQ**
BO32     *NQQIVGVHNAG***YSNGTINGGPKATAAFVEFINYAKAQ**
          .       .       .
          ab
MPR      TGQTAIAIHTN*****GGSSYNLGTRVTNDVFNNIQYWANQ**
AA513    SVDSMVAVHNAGYIVGGNREINGGPKIRRDFTNLFNQMN*****.
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Fig. 2 continued

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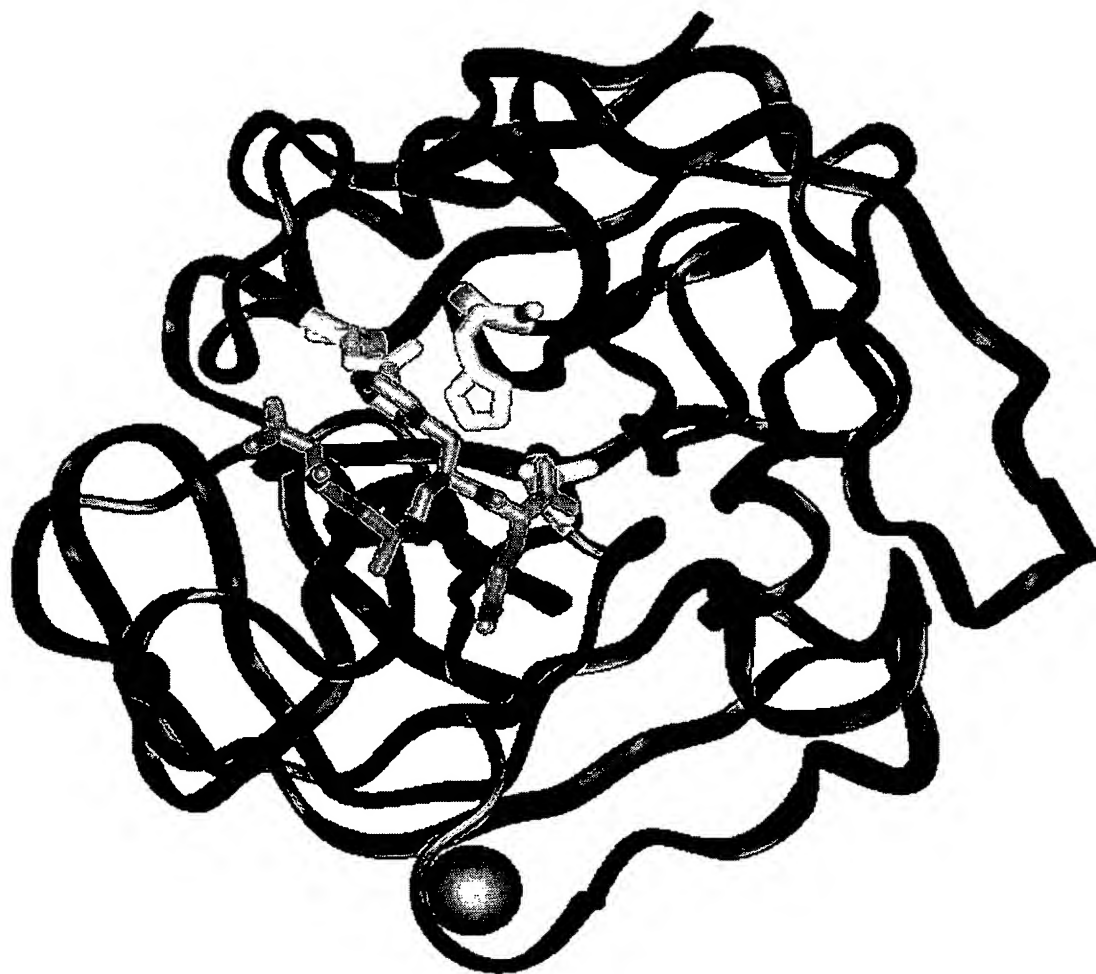


Fig. 3